

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/882,431DATE: 02/09/98
TIME: 11:29:54

INPUT SET: S23303.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

#4

SEQUENCE LISTING

ENTERED

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FEB 26 1998

PATENT SEQUENCE LISTING

PATENT SEQUENCE LISTING

1
2
3 (1) General Information:
4 (i) APPLICANT: Robert G. Ulrich,
5 Mark A. Olson
6 Sina Bavari
7
8 (ii) TITLE OF INVENTION: Bacterial Superantigen
9 Vaccines
10
11 (iii) NUMBER OF SEQUENCES:16
12
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: John Moran
15 (B) STREET: US Army MPMC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
16 (C) CITY: FORT DETRICK
17 (D) STATE: MARYLAND
18 (E) COUNTRY: USA
19 (F) ZIP: 21702-5012
20
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Floppy disk
23 (B) COMPUTER: Apple Macintosh
24 (C) OPERATING SYSTEM: Macintosh 7.5
25 (D) SOFTWARE: Microsoft Word 6.0
26
27 (vi) CURRENT APPLICATION DATA:
28 (A) APPLICATION NUMBER: 08/882,431
29 (B) FILING DATE: June 25, 1997
30 (C) CLASSIFICATION:
31
32 (vii) PRIOR APPLICATION DATA:
33 (A) APPLICATION NUMBER:
34 (B) FILING DATE:
35
36 (viii) ATTORNEY/AGENT INFORMATION:
37 (A) NAME: Moran, John
38 (B) REGISTRATION NUMBER: 26,313
39 (C) REFERENCE/DOCKET NUMBER:
40
41 (ix) TELECOMMUNICATION INFORMATION
42 (A) TELEPHONE: (301) 619-2065
43 (B) TELEFAX: (301) 619-7714
44
45 (2) INFORMATION FOR SEQ ID NO:1:
46 (i) SEQUENCE CHARACTERISTICS:

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47 (A) LENGTH: 830
48 (B) TYPE: Nucleic Acid
49 (C) STRANDEDNESS: Unknown
50 (D) TOPOLOGY: Unknown
51 (ii) MOLECULE TYPE: DNA
52 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
53
54 atgaaaaaaaa cagcatttac attactttta ttcattgccc 40
55
56 taacgttgac aacaagtcca cttgtaaatg gtagcgagaa 80
57
58 aagcgaagaa ataaatgaaa aagatttgcg aaaaaagtct 120
59
60 gaattgcagg gaacagcttt aggcaatctt aaacaaatct 160
61
62 attattacaa tgaaaaagct aaaactgaaa ataaagagag 200
63
64 tcacgatcaa tttcgacagc atactatatt gtttaaaggc 240
65
66 ttttttacag atcattcgtg gtataacgat ttattagtag 280
67
68 gttttgattc aaaggatatt gttgataaat ataaagggaa 320
69
70 aaaagtagac ttgtatggtg cttatgctgg ttatcaatgt 360
71
72 gcggggtggtg caccaaacaa aacagcttgt atgtatggtg 400
73
74 gtgtaacgtt acatgataat aatcgattga ccgaagagaa 440
75
76 aaaagtgccg atcaatttat ggctagacgg taaacaaaat 480
77
78 acagtacctt tggaaacggt taaaacgaat aagaaaaatg 520
79
80 taactgttca ggagttggat cttcaagcaa gacgttattt 560
81
82 acaggaaaaa tataatttat ataactctga tgtttttgat 600
83
84 gggaagggtc agaggggatt aatcgtgttt catacttcta 640
85
86 cagaaccctt gggttaattac gatttatttg gtgctcaagg 680
87
88 acagtattca aatacactat taagaatata tagagataat 720
89
90 aaaacgatta actctgaaaa catgcatatt gatatatatt 760
91
92 tatatacaag ttaaACATGG TAGTTTGTGAC CAACGTAATG 800
93
94 TTCAGATTAT TATGAACCGA GAATAATCTA 830
95
96 (2) INFORMATION FOR SEQ ID NO:2:
97 (i) SEQUENCE CHARACTERISTICS:
98 (A) LENGTH: 257
99 (B) TYPE: Amino Acid

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100 (C) STRANDEDNESS: Unknown
101 (D) TOPOLOGY: Unknown
102 (ii) MOLECULE TYPE: Peptide
103 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
104
105 Met Lys Lys Thr Ala Phe Thr Leu Leu Leu
106 1 5 10
107
108 Phe Ile Ala Leu Thr Leu Thr Thr Ser Pro
109 15 20
110
111 Leu Val Asn Gly Ser Glu Lys Ser Glu Glu
112 25 30
113
114 Ile Asn Glu Lys Asp Leu Arg Lys Lys Ser
115 35 40
116
117 Glu Lys Gln Gly Thr Ala Leu Gly Asn Leu
118 45 50
119
120 Lys Gln Ile Tyr Tyr Tyr Asn Glu Lys Ala
121 55 60
122
123 Lys Thr Glu Asn Lys Glu Ser His Asp Gln
124 65 70
125
126 Phe Arg Gln His Thr Ile Leu Phe Lys Gly
127 75 80
128
129 Phe Phe Thr Asp His Ser Trp Tyr Asn Asp
130 85 90
131
132 Leu Leu Val Arg Phe Asp Ser Lys Asp Ile
133 95 100
134
135 Val Asp Lys Tyr Lys Gly Lys Lys Val Asp
136 105 110
137
138 Leu Tyr Gly Ala Tyr Ala Gly Tyr Gln Cys
139 115 120
140
141 Ala Gly Gly Thr Phe Asn Lys Thr Ala Cys
142 125 130
143
144 Met Tyr Gly Gly Val Thr Leu His Asp Asn
145 135 140
146
147 Asn Arg Leu Thr Glu Glu Lys Lys Val Pro
148 145 150
149
150 Ile Asn Leu Trp Leu Asp Gly Lys Gln Asn
151 155 160
152

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153 Thr Val Pro Leu Glu Thr Val Lys Thr Asn
154                               165                170
155
156 Lys Lys Asn Val Thr Val Gln Glu Leu Asp
157                               175                180
158
159 Leu Gln Ala Arg Arg Tyr Leu Gln Glu Lys
160                               185                190
161
162 Tyr Asn Leu Tyr Asn Ser Asp Val Phe Asp
163                               195                200
164
165 Gly Lys Val Gln Arg Gly Leu Ile Val Phe
166                               205                210
167
168 His Thr Ser Thr Glu Pro Ser Val Asn Tyr
169                               215                220
170
171 Asp Leu Phe Gly Ala Gln Gly Gln Tyr Ser
172                               225                230
173
174 Asn Thr Leu leu Arg Ile Tyr Arg Asp Asn
175                               235                240
176
177 Lys Thr Ile asn Ser Glu Asn Met His Ile
178                               245                250
179
180 Asp Ile Tyr Leu Tyr Thr Ser
181                               255
182

```

183 (2) INFORMATION FOR SEQ ID NO:3:

184 (i) SEQUENCE CHARACTERISTICS:

185 (A) LENGTH: 757

186 (B) TYPE: Nucleic Acid

187 (C) STRANDEDNESS: Unknown

188 (D) TOPOLOGY: Unknown

189 (ii) MOLECULE TYPE: DNA

190 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

191
192 atgagaaaag cgaagaaata aatgaaaaag atttgcgaaa      40
193
194 aaagtctgaa ttgcagggaa cagctttagg caatcttaaa      80
195
196 Caaatctatt attacaatga aaaagctaaa actgaaaata     120
197
198 aagagagtca cgatcaattt cgacagcata ctatattggt     160
199
200 taaaggcttt ttacagatc attcgtggta taacgattta     200
201
202 ttagtacgtt ttgattcaaa ggatattggt gataaatata     240
203
204 aagggaaaaa agtagacttg tatggtgctt atgctggtta     280
205

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206 tcaatgtgcg ggtggtacac caaacaaaac agcttgtatg 320
207
208 tatggtggtg taacgttaca tgataataat cgattgaccg 360
209
210 aagagaaaaa agtgccgatac aatttatggc tagacggtaa 400
211
212 acaaaatata gtacctttgg aaacgggttaa aacgaataag 440
213
214 aaaaatgtaa ctgttcagga gttggatctt caagcaagac 480
215
216 gttattttaca ggaaaaatat aatttatata actctgatgt 520
217
218 ttttgatggg aaggttcaga ggggattaat cgtgtttcat 560
219
220 acttctacag aaccttcggt taattacgat ttatttggtg 600
221
222 ctcaaggaca gtattcaaat acactattaa gaatatatag 640
223
224 agataataaaa acgattaact ctgaaaacat gcatattgat 680
225
226 atatattttat atacaagtta aACATGGTAG TTTTGACCAA 720
227
228 CGTAATGTTT AGATTATTAT GAACCGAGAA TAATCTA 757
229
230 (2) INFORMATION FOR SEQ ID NO:4:
231 (i) SEQUENCE CHARACTERISTICS:
232 (A) LENGTH:233
233 (B) TYPE: Amino Acid
234 (C) STRANDEDNESS: Unknown
235 (D) TOPOLOGY: Unknown
236 (ii) MOLECULE TYPE: Peptide
237 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
238
239 Met Glu Lys Ser Glu Glu Ile Asn Glu Lys
240 5 10
241
242 Asp Leu Arg Lys Lys Ser Glu Lys Gln Gly
243 15 20
244
245 Thr Ala Leu Gly Asn Leu Lys Gln Ile Tyr
246 25 30
247
248 Tyr Tyr Asn Glu Lys Ala Lys Thr Glu Asn
249 35 40
250
251 Lys Glu Ser His Asp Gln Phe Arg Gln His
252 45 50
253
254 Thr Ile Leu Phe Lys Gly Phe Phe Thr Asp
255 55 60
256
257 His Ser Trp Tyr Asn Asp Leu Leu Val Arg
258 65 70

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SEQUENCE VERIFICATION REPORT
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